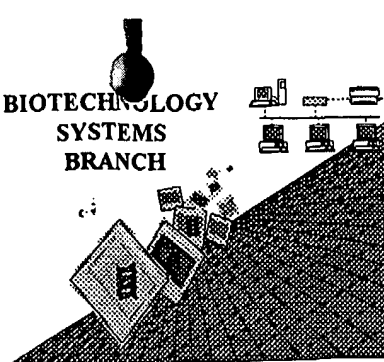


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



✓ 0400
5-9-01.

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/833,222

Source: OIPF

Date Processed by STIC: 4/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/833,222

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
 (i) **SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) **SEQUENCE DESCRIPTION:SEQ ID NO:X:**
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,222

DATE: 04/30/2001

TIME: 08:01:23

Input Set : A:\a2d-4SEQ.txt

Output Set: N:\CRF3\04302001\I833222.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Qin, Ning
 5 Codd, Ellen
 7 <120> TITLE OF INVENTION: cDNA encoding the Calcium Channel Alpha2Delta-4 Subunit
 9 <130> FILE REFERENCE: calcium channel alpha2delta-4 subunit
 OK 11 <140> CURRENT APPLICATION NUMBER: US/09/833,222
 12 <141> CURRENT FILING DATE: 2001-04-11
 E--> 14 <160> NUMBER OF SEQ ID NOS: 10 14 (see below)
 16 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

448 <210> SEQ ID NO: 13
 449 <211> LENGTH: 188 105 shown below
 450 <212> TYPE: DNA
 451 <213> ORGANISM: Homo sapiens
 453 <400> SEQUENCE: 13
 454 gagaatgccc aggactgcgg cggcgcctcg gacacctcag cctcgccgcc cctactcctg 60
 E--> 456 ctgcctgtgt gtgcctgggg gctactgccq caactcctgc ggtga 105
 460 <210> SEQ ID NO: 14
 461 <211> LENGTH: 58 35 shown
 462 <212> TYPE: PRT
 463 <213> ORGANISM: Homo sapiens
 465 <400> SEQUENCE: 14
 466 Glu Asn Ala Gln Asp Cys Gly Gly Ala Ser Asp Thr Ser Ala Ser Ser Pro
 467 1 5 10 15
 469 Pro Leu Leu Leu Leu Pro Val Cys Ala Trp Gly Leu Leu Pro Gln Leu
 E--> 470 20 20 25 25 30 30
 E--> 472 Leu Arg 35

last sequence in file
 FYI - Per 1.822
 of sequence
 Rule, a MAXIMUM
 of 16 amino
 acids
 per line
 allowed
 misaligned amino acid nos. - see item 4 on
 Error Summary
 Sheet

VERIFICATION SUMMARY

DATE: 04/30/2001

PATENT APPLICATION: US/09/833,222

TIME: 08:01:24

Input Set : A:\a2d-4SEQ.txt

Output Set: N:\CRF3\04302001\I833222.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:456 M:252 E: No. of Seq. differs, <211>LENGTH:Input:188 Found:105 SEQ:13
L:470 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:472 M:252 E: No. of Seq. differs, <211>LENGTH:Input:58 Found:35 SEQ:14
L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (10) Counted (14)